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Query Match      4.9%  Score 45.41  DB 1:  Length 3618;
Best Local Similarity 53.0%  Pred. NO. 0.0026;
Matches 97;  Conservative 0;  Mismatch 86;  Indels 0;  Gaps 0;

QY 257 TTAAGTAGGCTTTGAAATGCAATAAACATAATAGTTAGTGTAAATGTTAGTCAAA 316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2459 TAAATTAAGCTTAAATTAACCTAAATTTTAAATATATGTAAATAAATTTTAAATAAAT 2930

QY 417 TTAATAGCAAAATAAGTAGCTAGCTAATTAACCAAAATAAATTAAGTTATAGT 376
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2899 TTAATAATTAATAATAATAATATGTTAAATTTAAATTTAAATTTAAATTTAAAT 2840

QY 477 TAAATTAATAGTGGCTGTTGATGCTCAACTAATTTTACCCACTAATTTTATCT 436
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Db 2839 TTAATAATAATGTTAAATTTTAAATAAATTTTAAATAAATTTTAAATGCTGTATCTAT 2780

QY 437 TTA 439
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Db 2779 ATA 2777

RESULT 4
US 08 750-457 745
Sequence 7, Application US/83753377
Patent No. 608437
GENERAL INFORMATION:
APPLICANT: KREBBERS, Edm
APPLICANT: WILLIAMS, Mark
APPLICANT: LEHMAN, JED
TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
TITLE OF INVENTION: MALE STERILE PLANTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DWANE, SWICKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22413-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTN PATENT SOURCE: US/83753377
FILING DATE: 21-MAR-1997
CLASSIFICATION: B00
ACTORNEL/ACN INFORMATION:
NAME: Macosko, Malcolm K.
REGISTRATION NUMBER: 69,300
REFERENCE/DOCKET NUMBER: 018030-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4187 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Ecoli-HindIII region of plasmid pCol13
FEATURE:
NAME/KEY: prim_transcript
LOCATION: 188
FEATURE:
NAME/KEY: exon
LOCATION: 188..212
FEATURE:
NAME/KEY: intron
LOCATION: 213..556

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FEATURE:
NAME/KEY: exon
LOCATION: 557..718
FEATURE:
NAME/KEY: intron
LOCATION: 719..1224
FEATURE:
NAME/KEY: exon
LOCATION: 1226..2771
OTHER INFORMATION: Exon_start 2
OTHER INFORMATION: Exon_end 2771
OTHER INFORMATION: Note: "Exon continues up to the polyadenylation site"
FEATURE:
NAME/KEY: CDS
LOCATION: 576..718
FEATURE:
NAME/KEY: CDS
LOCATION: 1226..2771
FEATURE:
NAME/KEY:
LOCATION: 1269..2771
OTHER INFORMATION: Note: "Intron end is polyadenylated"
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 2772..4137
FEATURE:
NAME/KEY:
LOCATION: 1..6
OTHER INFORMATION: /label Exon1
FEATURE:
NAME/KEY:
LOCATION: 11..16
OTHER INFORMATION: /label Xba1
FEATURE:
NAME/KEY:
LOCATION: 45..50
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LOCATION: 265..270
OTHER INFORMATION: /label HindIII
FEATURE:
NAME/KEY:
LOCATION: 329..334
OTHER INFORMATION: /label Xba1
FEATURE:
NAME/KEY:
LOCATION: 835..840
OTHER INFORMATION: /label BamHI
FEATURE:
NAME/KEY:
LOCATION: 1269..1274
OTHER INFORMATION: /label Hind
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NAME/KEY:
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OTHER INFORMATION: /label HindIII
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NAME/KEY:
LOCATION: 2884..2889
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FEATURE:
NAME/KEY:
LOCATION: 2828..2833
OTHER INFORMATION: /label HindIII
FEATURE:
NAME/KEY:
LOCATION: 4114..4119
OTHER INFORMATION: /label SalI
FEATURE:
NAME/KEY:
LOCATION: 4132..4137

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? CURRENT APT : ALL-04 QIPDOW 87965570-367C
? CURRENT FILING DATE: 2000-05-05
? PRIOR APPLICATION NUMBER: US 60/064,764
? PRIOR FILING DATE: 1997-11-07
? NUMBER OF SEQ ID NOS: 22
? SOFTWARE: Patent In Version 3.0
? SEQ ID NO 1
? LENGTH: 2791
? TYPE: DNA
? ORGANISM: Mus musculus
US-09-570-367C 1

Query Match      4.1% Score 38; DB 4; Length 2746
Best Local Similarity    89.1%; Pctd.No. 0.29; 5; Indels
Matches 41; Conservative 0; Mismatches

QY   1 A'ATAGACGCACTGTGGTCAGCGGCAGCGGCAGTGAATTGTG 46
     |||||
DB    2791 A'TAAGCACACTGTGGTCAGACGCCGCGTGCTGCTGCTAGTAG 2746

RESULT 11
US 08 905-224-37
Sequence 37 ; Application 255,33 or 223
Patent No. 6,220,294
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Bactrix, Asymetric
INVENTOR: Bactrix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 504
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knabbe, Martens, Olson & Bear
STREET: 501 West Broadway
CLTY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-4505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPILED BY IBM PC COMPATIBLE
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/065,223
FILING DATE:
CLASSIFICATION: 536
AUTHORITY/AGENT INFORMATION:
NAME: LSAIOLSON, Ncd A.,
REGISTRATION NUMBER: 29,655
REFERENCE/PACKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 555 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: Genomic DNA
FEATURES:
NAME/KEY: promoter
LOCATION: 1..500
FEATURE:
NAME/KEY: transcription start site
LOCATION: 501
FEATURE:
NAME/KEY: TF binding-site
LOCATION: 191..206
IDENTIFICATION METHOD: mat inspector prediction
OTHER INFORMATION: name ARNT_01
OTHER INFORMATION: score 0.964
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? LOCATION: complement(460..470)
? IDENTIFICATION METHOD: matInspector prediction
? OTHER INFORMATION: name APL_Q4
? OTHER INFORMATION: score 0.963
? OTHER INFORMATION: sequence AGTACTGGAAG
? FEATURE:
? NAME/KEY: protein_bind
? LOCATION: complement(460..470)
? IDENTIFICATION METHOD: matInspector prediction
? OTHER INFORMATION: name APL_Q2
? OTHER INFORMATION: score 0.961
? OTHER INFORMATION: sequence AGTACTGGAAG
? FEATURE:
? NAME/KEY: protein_bind
? LOCATION: 547..555
? IDENTIFICATION METHOD: matInspector prediction
? OTHER INFORMATION: name PADSC
? OTHER INFORMATION: score 1.800
? OTHER INFORMATION: sequence TGKATGTC
US 08 905,224-47

Query Match 4.1k; Score 37.8; DB 4; Length 555;
Best local Similarity 86.7%; Pred. No. 0.18;
Matches 49; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 CTATAGGACGCGTGGTACGAGCGGCTGGTGGTATTTGG 46
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DB 1 CTATAGGACGCGKGGTGGAGCGGCGGCTGGTGGTGTGTR 45

RESULT 12
US 09 247 155-47
? Sequence 37, Application US/09247.55A
? Patent No. 6,612,922
? GENERAL INFORMATION:
? APPLICANT: Dumas Milne Edwards, Jean Baptiste
? APPLICANT: Duclert, Aymeric
? APPLICANT: Bouasse-Lerret, Lydie
? TITLE OF INVENTION: Complementary DRAs
? FILE REFERENCE: GENSEI/021A
? CURRENT APPLICATION NUMBER: 65,542,157
? CURRENT FILING DATE: 1999-02-09
? EARLIER APPLICATION NUMBER: 62,074,121
? EARLIER FILING DATE: 1998-02-09
? EARLIER APPLICATION NUMBER: 60,081,563
? EARLIER FILING DATE: 1998-04-13
? EARLIER APPLICATION NUMBER: 60,096,116
? EARLIER FILING DATE: 1998-08-10
? EARLIER APPLICATION NUMBER: 60,096,275
? EARLIER FILING DATE: 1998-10-04
? NUMBER OF SEQ ID NOS: 182
? SOFTWARE: Patent-fm
? SEQ ID NO 47
? LENGTH: 555
? TYPE: DNA
? ORIGINATOR: Hawk, Jacques
? FEATURE:
? NAME/KEY: promoter
? LOCATION: 1..500
? FEATURE:
? OTHER INFORMATION: codon_start "501"
? FEATURE:
? NAME/KEY: protein_bind
? LOCATION: 191..206
? OTHER INFORMATION: matInspector prediction
? OTHER INFORMATION: name APL_Q1
? OTHER INFORMATION: score 0.964
? OTHER INFORMATION: sequence aaacacacatctact
? FEATURE:
? NAME/KEY: protein_bind
? LOCATION: 193..204
? OTHER INFORMATION: matInspector prediction
? OTHER INFORMATION: name APL_Q4
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? FEATURE:
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? OTHER INFORMATION: score 0.965
? FEATURE:
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? OTHER INFORMATION: score 0.985
? OTHER INFORMATION: sequence aaacacatctact
? FEATURE:
? NAME/KEY: protein_bind
? LOCATION: complement(193..204)
? OTHER INFORMATION: matInspector prediction
? OTHER INFORMATION: name USP_01
? OTHER INFORMATION: score 0.985
? OTHER INFORMATION: sequence aaacacatctact
? FEATURE:
? NAME/KEY: protein_bind
? LOCATION: complement(193..204)
? OTHER INFORMATION: matInspector prediction
? OTHER INFORMATION: name NMTC_01
? OTHER INFORMATION: score 0.956
? OTHER INFORMATION: sequence aaacacatctact
? FEATURE:
? NAME/KEY: protein_bind
? LOCATION: 195..202
? OTHER INFORMATION: matInspector prediction
? OTHER INFORMATION: name USP_01
? OTHER INFORMATION: score 0.997
? OTHER INFORMATION: sequence aaacacatctact
? FEATURE:
? NAME/KEY: protein_bind
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? OTHER INFORMATION: matInspector prediction
? OTHER INFORMATION: name USP_01
? OTHER INFORMATION: score 0.991
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? NAME/KEY: protein_bind
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? OTHER INFORMATION: name BZFL_01
? OTHER INFORMATION: score 0.963
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? FEATURE:
? NAME/KEY: protein_bind
? LOCATION: 307..310
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? OTHER INFORMATION: name ELK1_02
? OTHER INFORMATION: score 0.963
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? FEATURE:
? NAME/KEY: protein_bind
? LOCATION: 450..459
? OTHER INFORMATION: matInspector prediction
? OTHER INFORMATION: name CETS1P54_01
? OTHER INFORMATION: score 0.974
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? FEATURE:
? NAME/KEY: protein_bind
? LOCATION: complement(460..470)
? OTHER INFORMATION: matInspector prediction
? OTHER INFORMATION: name APL_Q4
? OTHER INFORMATION: score 0.963
? OTHER INFORMATION: sequence aaacacatctact
? FEATURE:

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: 0509231795A
3 FILING DATE: 27 JUN-1997
4 CLASSIFICATION: 435
5 AUTHORITY/AGENCY INFORMATION:
6 NAME: Gravello, Michelle
7 REGISTRATION NUMBER: 40,261
8 REFERENCE/KEY NUMBER: 7841-062
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: (416) 364 7411
11 TELEFAX: (416) 361-1398
12 INFORMATION FOR SEQ ID NO: 36:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 665 base pairs
15 TYPE: nucleic acid
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 MOLECULE TYPE: cDNA
19 ORGANISM: Homo sapiens
20 IMMEDIATE SOURCE:
21 CLONE: Rb 32
22 US 08 883 795A 36

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Query Match: 4.08; Score 37.4; DB 2; Length 665;
Best Local Similarity 47.38; Pred. No. 1.25; Mismatches 126; Indels 0; Gaps 0;
Matches 113; Conservative 0;

QY 210 TCTACATTTCATTCGACATATGATGAACTAAATTTATGGCACTTAAGGAGCTGT 269
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 283 TATAAA*ATTTAATATATAAAATATTTAAITATAAATATTTTAATTAATAATATTTAAT 224

QY 270 TGAATGCAATAAATACTAATAGTAGTGGCTAATAATCTTAGCGAAATATCTAGCTAAC 329
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DB 224 TATAAATATTTAATATATAAAATATTTAAITATAAAATATTTAATTAATAAATATTTAAI 164

QY 330 AAATACCTACCTAACTATTAACTAATTTACCAAAATAAATCTATAGTTAAATTAATAGT 389
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DB 163 TATAAAGATTTAATATATAAATATTTAACTATAAATATTTTAATTAATAATATTTAAI 104

QY 390 TGGAGCTGTTGAAAGCTTCAATTAATTTAAGCAATAAGCTTTATCTTTAGTGGCAATCA 448
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 103 TATAAATATTTAATATATAAATATTTAAITATAAATATTTTAATTAATAAATATTTTAA 45

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Search completed: December 30, 2002, 21:27:52
Job Time : 82 secs

US-09-323-195A-3
 ; Sequence 3, Application US/09323195A
 ; Patent No. 6462257
 ; GENERAL INFORMATION:
 ; APPLICANT: Pullman, Gerald
 ; APPLICANT: Cairney, John
 ; APPLICANT: Perrera, Ranjan
 ; TITLE OF INVENTION: VICILIN-LIKE SEED STORAGE PROTEIN GENE PROMOTER AND
 ; TITLE OF INVENTION: METHODS OF USING THE SAME
 ; FILE REFERENCE: IPSTG006
 ; CURRENT APPLICATION NUMBER: US/09/323,195A
 ; CURRENT FILING DATE: 1999-06-01
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 340
 ; TYPE: LNA
 ; ORGANISM: Pinus taeda
 US-09-323-195A-3

Query Match 4.2%; Score 39; Ds 4; Length 340;
 Best Local Similarity 89.4%; Pred. No. 0.067;
 Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Q7 1 ACTATAGGACACGGTGGTGGACGGCCCGGGTGGTATTGGT 47
 Db 1 ACTATAGGACACGGTGGTGGACGGCCCGGGTGGTAAAGTGGT 47

[illegible]


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SOURCE
  2000007
  2 (bases 1 to 4285)
  Direct Submission
  TITLE
  Journal
  Submitted (24-MAY-1994) Young-Kwan Jin, Biological Sciences, Purdue
  University, 439 Busson Life Science Research Building, West
  Lafayette, IN 47907, USA
  FEATURES
    location/qualifiers
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    TDFFPRLPHVSLAHDFQMLASAVYLOVSTLSQALFVTRSRWSVFRPGLQSA
    FLVAGIATILAVVANVAIAAKKIQKQWACVIMVNYICVLLDILKFLRAISGR
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[illegible]

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		1947..2078					
intron		/gene="PHY1"					
		/number=1					
		2079..4403					
exon		/gene="PHY1"					
		/number=2					
		2097..4426					
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		/evidence="Hydrolysis of phytin"					
		/codon_start=1					
		/evidence="experimental"					
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ORIGIN							
		Query Match		9.98; Score 89.2; DB 8; Length 4695;			
		Best Local Similarity		72.18; Prod. No. 8.9e-11;			
		Matches 100; Conservative		0; Mismatches 51; Indels 9; Gaps 3;			
257		TTAAGAGACGCTTGAAAGCAATAAAACAATAGTAGTTCGTCAAAATTGT--TATGGA		314			
1071		TTTAGAGCTGCTTGAAAGCAATAGTAGTTCGTCAAAATTGT--TATGGA		1140			
315		AATTATCTAGCTAACAATAGTACCTAAN--TATTAACCTAATTAGCAAAAATACCTATA		374			
1131		AATTAGCTAACAATAAATAGTTAGTACAGAGTACTAATTTACTAAAAATAGTTATA		1190			
375		GTTAAATATTAAGT----TGGTGTGTTTGAATGCTCAACTAATTTAGGCTAACT		429			
1191		GCTAAGCATATATATAGCTATAGAGGTGTGTGGATGCTCTACTAATTT--TACTA		1248			
440		TTTATCTTACTGCAATCAACAAGGCAATAGCTTACTGCTTC		471			
1249		ATTATCTAGTCAATCAATAAATAGCTTATATGTCATTAG		1290			
REFSeq 9							
LOCUS		AF434193					
DEFINITION		Zea mays: 11000192 v1 (c1) gene, 51 kb, 5' UTR, 5' UTR, 5' UTR		linear		PLN 08-MAY-2002	
ACCESSION		AF434193					
VERSION		AF434193.1					
KEYWORDS		GI:20502804					
SOURCE		Zea mays					
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta					


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SELSYKNDKEETLPSSTLASHLQSTDTFTTGRGRALQSSGRLARLQNR
KMAVADQQTQSAIQIIFAKQELLEDTNKKQNSDSSYAVKAKTIGVLLNDF
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KNKLFNRDLN"
cds
complement(11355, 11627)

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Query Match
Best Local Similarity 51.4% Score 48.4; DB 1; Length 18101;
Matches 112; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 186 TTGATTCCTTCCTTGAGACACIGILCTATATATTCATTGGCGATATGATGAATAAA 245
DB 17813 TTAAAFCTTTAAAGCGCGATTTCTAACIAVYVDTGTATATTTAGAAATTA 17754

QY 246 TTAATGGACAGGCTTGAAGCAATAAACTAAATAGTTAGTGGCTAAAAA 305
DB 17753 ATGAATGAAGCTGCTATACATTTTGAAGCTTATAATATGATATAATGATAGAAAT 17694

QY 306 TCTAGTGAATATATCTAGCTAAVAAATACATCTACTAACTAATTAATACTAAAT 365
DB 17693 ATGCAATTAATAATATTAACACGACCAAAATACATTAACCAATAATAATAATA 17634

QY 366 TAAATTAATAGTAAATATTAAGTTGGGCTGCTTGAAT 403
DB 17633 CTAATCATAGTTAAATAATATATCTGCAATTAATGAAT 17596

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Search completed: December 30, 2002, 22:17:41
Job time: 2998 secs

|||||
DB 385 AAAATTCATCTAGATCAGAGCTAAAGTTGTGGAGGCT 431

Search completed: December 30, 2002, 23:50:17
Job time : 2160 secs

Result No.	Score	Query			ID	Description
		Match	Length	DB		
c 1	40.6	4.4	2000	9	US-09-948-842A-5404	Sequence 5309, Ap
c 2	40.2	4.3	640681	13	US-09-790-988-1	Sequence 1, Appli
c 3	39.8	4.3	1188	1	US-10-051-407-5	Sequence 5, Appli
c 4	38.6	4.2	334	10	US-09-969-474-197	Sequence 197, App
c 5	38.6	4.2	334	10	US-09-969-474-198	Sequence 198, App
c 6	38.2	4.1	1175	9	US-10-051-407-4	Sequence 4, Appli
c 7	38	4.1	2791	9	US-09-617-278-1	Sequence 1, Appli
c 8	38	4.1	2791	10	US-09-945-524-1	Sequence 1, Appli
c 9	38	4.1	2791	10	US-09-944-634-1	Sequence 1, Appli
c 10	37.8	4.1	2154	10	US-09-811-094-43	Sequence 43, Appli
c 11	37.6	4.1	985	10	US-09-811-094-44	Sequence 44, Appli
c 12	37.6	4.1	1872	9	US-09-933-812A-604	Sequence 404, Ap
c 13	37.6	4.1	53332	10	US-09-801-361-3	Sequence 3, Appli
c 14	37.4	4.0	643631	10	US-09-706-698-1	Sequence 1, Appli
c 15	37.2	4.0	2611	9	US-09-891-139A-1	Sequence 1, Appli
c 16	37.2	4.0	2745	9	US-09-891-095-540	Sequence 340, App
c 17	37	4.0	2000	9	US-09-948-842A-4650	Sequence 4650, Ap
c 18	37	4.0	2240	10	US-09-811-232-1	Sequence 1, Appli
c 19	36.6	4.0	594	9	US-09-986-114-16	Sequence 16, Appli



CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 600 bp; 177 A; 97 C; 110 G; 215 T; 1 other;

Query Match 4.6%; Score 42.6; DB 23; Length 600;
 Best Local Similarity 54.9%; Field No. 0.11;
 Matches 6; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 243 TGAAGAA TAAATATGCGACCTAAGGAGGTGTTCAATGCAATAAAGCTAAATAGTT 292
 DB 496 TGAAGCAATGTTTAAATTCCTTTTCAAGAAAGAAAGAAAGAAAGAAAGAAAG 437
 QY 293 AATGCTAAATATGTAAGCAATATGCAATGCAATGCAATGCAATGCAATGCAAT 352
 DB 436 TCTTTCTATATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 477
 QY 453 AATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 510
 DB 476 AGAATACAAAGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 544

RESULT 1:

AP070162:
ID AB070162 standard: DNA: 18817 bp.

AC ABL44495:
ID AB070162:

01 JUN 2002 (first entry)

Chemically treated cell signalling DNA sequence complementary to #26.

Cell signalling; cytosine methylation; cell signalling disease;

cytostatic; cytostatic; ds.

Unidentified.

W0203202807 A2.

10 JAN 2002.

29 JUN 2001; z001W0-EP07471.

30 JUN 2000; 2000DE-1042529.

01 SEP 2000; 2000DE-1043826.

(EP16-) EP16GENOMICS AG.

01ek A. Piepenbrock C. Notlin K.

WPI: 2002-154759/20.

Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling.

claim 1: Seq ID No 52; 24pp-sequence listing: English.

The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pre-treated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell

CC signalling, as well as cytosine methylation and/or DNA methylation for
 CC detecting cytosine methylation, as well as a method which is
 CC particularly suitable for the diagnosis and/or therapy of cancer, as
 CC epigenetic parameters of genes associated with cell signalling, the
 CC chemically modified DNA provided by the invention is useful for diagnosis
 CC and therapy of diseases such as solid tumors and cancer, the sequences
 CC given in records AB070162-AB070166 represent chemically pre-treated
 CC genomic DNA's of genes associated with cell signalling.
 CC Note: The sequence data for this patent is not reproduced in the printed
 CC specification, but is based on sequence information supplied by the
 CC European Patent Office.

XX Sequence 18817 bp; 5486 A; 156 C; 3507 G; 9576 T; 1 other;

Query Match 4.6%; Score 42.6; DB 24; Length 18817;
 Best Local Similarity 48.2%; Field No. 6.45;
 Matches 120; Conservative 0; Mismatches 8; Indels 0; Gaps 1;
 QY 218 TTTCATTCGACGATAGTATGATTAATTAATTAATTAATTAATTAATTAATTAAT 277
 DB 12942 TTTTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1
 QY 278 AATAAATTAATAGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 2873
 DB 12879 AATAAATTAATAGTATGATTAATTAATTAATTAATTAATTAATTAATTAAT 1 457
 QY 338 AATTAATTAATAGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 497
 DB 12812 AATAAATTAATAGTATGATTAATTAATTAATTAATTAATTAATTAATTAAT 1 12812
 QY 358 TTCAAGGCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 497
 DB 12762 AATAAATTAATAGTATGATTAATTAATTAATTAATTAATTAATTAATTAAT 1 12762
 QY 458 TAAAGTAA 466
 DB 12692 AATAAATTAAT 12684

RESULT 14

ABL44495:

3D ABL44495 standard: DNA: 18817 bp

XX ABL44495:

26-MAR-2002 (first entry)

Human metastasis associated gene SEQ ID NO 18.

Metastasis associated gene; cytosine methylation; gene; ds.

Human sapiens.

W020017476 A2.

18-OCT-2001.

06-APR-2001; 2001W0-EP06970.

06-APR-2000; 2000DE-1019058.

07-APR-2000; 2000DE-1019173.

30-JUN-2000; 2000DE-1032529.

31-SEP-2000; 2000DE-1043826.

(EP16-) EP16GENOMICS AG.

01ek A. Piepenbrock C. Notlin K.

WPI: 2002-154720/1.

New nucleic acid derived from chemically treated metastasis genes, useful for diagnosis of cancers by analysis of cytosine methylation

